PATENT
Attorney Docket No. **CASE-06816**

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of: Evan Samuel Deneris *et al.*
Serial No.: 10/027,859 Group No.: 1653
Filed: 10/25/01 Examiner:
Entitled: **Reagents And Methods For The Screening Of Compounds Useful In The Treatment Of Neurological Diseases**

PRELIMARY AMENDMENT

Assistant Commissioner for Patents
Washington, D.C. 20231

CERTIFICATE OF MAILING UNDER 37 C.F.R. § 1.8(a)(1)(i)(A)

I hereby certify that this correspondence (along with any referred to as being attached or enclosed) is, on the date shown below, being deposited with the U.S. Postal Service with sufficient postage as first class mail in an envelope addressed to: Assistant Commissioner for Patents, Washington, D.C. 20231.

Dated: April 12, 2002 By: Christopher J. Collins

Sir or Madam:

REMARKS

The Applicants submit the following amendments pursuant to provisions in 37 CFR § 1.312. In this instance, the "amendment" consists of "an amendment to the Specification" as described in MPEP § 714.16(A). The amendment does not introduce any new matter.

A clean version of the rewritten and added paragraphs to the specification with instructions for entry pursuant to 37 C.F.R. § 1.121(b)(1)(ii) is included beginning on page two of this communication. A marked-up version of the rewritten paragraphs pursuant to 37 C.F.R. § 1.121(b)(1)(iii) is attached as Appendix I.

PATENT
Attorney Docket No. **CASE-06816**

CLEAN VERSION OF REWRITTEN AND ADDED PARAGRAPHS
PURSUANT TO 37 CFR § 1.21 (b)(1)(ii)

IN THE SPECIFICATION:

Please insert the following paragraph in the specification:

Insert the following language as the first paragraph in that portion of the specification relating to the "Description Of The Figures" (Page 12, Before line 15).

--The file of this patent contains at least one drawing executed in color. Copies of this patent with color drawing(s) will be provided by the Patent and Trademark Office upon request and payment of necessary fees.--

The following amendment is offered to harmonize the reference to highlighted elements in a Formal Drawing (e.g. Figure 1) with the description of this same Figure in the Specification.

Please replace the paragraph beginning at page 12, line 15, and ending on page 12, line 24, with the following rewritten paragraph:

--Figure 1 shows the nucleotide sequence (SEQ ID NO:1) of the λ73 cDNA and the deduced primary structure of Pet-1 (SEQ ID NO:2). The two sets of numbering on the right mark either the nucleotide sequence or amino acid residues. Translation termination codons flanking the open reading frame are marked by asterisks. The ETS domain is contained within the dashed lines. Underlined amino-acid sequences within the ETS domain mark homologous region in other ETS-domains that were used to prepare primers for the degenerate PCR screen. Boxed residues indicate putative MAP kinase phosphorylation sites. A putative nucleotide binding P-loop is enclosed by an oval. A possible polyadenylation signal motif is shown in capital letters at the end of the nucleotide sequence.--

The following amendment is offered to harmonize the reference to highlighted elements in a Formal Drawing (e.g. Figure 2A) with the description of this same Figure in the Specification.

Please replace the paragraph beginning at page 12, line 25, and ending on page 13, line 5, with the following rewritten paragraph:

-- Figure 2 show the alignment of various ETS-domain sequences. A) The first three letters of each ETS-domain factor designation shown on the left indicate an organism, e.g. DRO, *Drosophila melanogaster*, followed by the common gene name. Columns of more than 40% sequence identity are in bold text. B) Parsimony analysis of sequences encoding different ETS domains. The phylogenetic tree demonstrates relative similarities among the ETS DNA binding domains of Pet-1, Ets-1 and members of the ERG subfamily. The available sequence for the Drosophila ETS-3 ETS domain is incomplete (Chen, T., *et al.*, "Isolation and characterization of five Drosophila genes that encode an ets-related DNA binding domain" *Dev. Biol.* 151:176-191, 1992). Branch lengths do not represent estimates of evolutionary distances between protein sequences.--

CONCLUSION

This amendment to the Specification does not introduce new matter and will not require an additional search of the prior art by the Examiner. Therefore, the Applicants respectfully request the examiner to make it of record in the instant application. Should the Examiner have any additional questions or comments, the Applicants encourage the Examiner to call the undersigned collect at (617) 252-3353.

Dated: April 12, 2002

Thomas W. Brown
Registration No. 50,002

MEDLEN & CARROLL, LLP
101 Howard Street, Suite 350
San Francisco, California 94105

Application No.: 10/027,859 Filed: 10/25/01

APPENDIX I

VERSION WITH MARKINGS TO SHOW CHANGES MADE PURSUANT TO 37 CFR § 1.12(b)(iii)

In the Specification:

Paragraph beginning at page 12, line 15 has been amended as follows:

Figure 1 shows the nucleotide sequence (SEQ ID NO:1) of the λ73 cDNA and the deduced primary structure of Pet-1 (SEQ ID NO:2). The two sets of numbering on the right mark either the nucleotide sequence or amino acid residues. Translation termination codons flanking the open reading frame are marked by asterisks. The ETS domain is [shaded] contained within the dashed lines. Underlined amino-acid sequences within the ETS domain mark homologous region in other ETS-domains that were used to prepare primers for the degenerate PCR screen. Boxed residues indicate putative MAP kinase phosphorylation sites. A putative nucleotide binding P-loop is enclosed by an oval. A possible polyadenylation signal motif is shown in capital letters at the end of the nucleotide sequence.

Paragraph beginning at page 12, line 25 has been amended as follows:

Figure 2 show the alignment of various ETS-domain sequences. A) The first three letters of each ETS-domain factor designation shown on the left indicate an organism, e.g. DRO, *Drosophila melanogaster*, followed by the common gene name. Columns of more than 40% sequence identity are [shaded]in bold text. B) Parsimony analysis of sequences encoding different ETS domains. The phylogenetic tree demonstrates relative similarities among the ETS DNA binding domains of Pet-1, Ets-1 and members of the ERG subfamily. The available sequence for the Drosophila ETS-3 ETS domain is incomplete (Chen, T., *et al.*, "Isolation and characterization of five Drosophila genes that encode an ets-related DNA binding domain" *Dev. Biol.* 151:176-191, 1992). Branch lengths do not represent estimates of evolutionary distances between protein sequences.